

## SPECIFICATION AMENDMENTS

1. Please replace the paragraph beginning at line 11 on page 13 and ending at line 16 on page 13 with the following rewritten paragraph:

In one embodiment of the present invention, there is provided an isolated nucleic acid corresponding to a promoter isolated from a sugarcane stem-regulated, defense-inducible gene, designated o-methyl transferase (OMT) promoter, having the sequence of nucleotides -3012 to -1 as depicted in FIGURE 1 (nucleotides 1 to 3012 of SEQ ID NO:1).

2. Please replace the paragraph beginning at line 25 on page 14 with the following rewritten paragraph:

In a specific embodiment of the present invention, the OMT promoter includes nucleotides -3012 to -1 of FIGURE 1 (nucleotides 1 to 3012 of SEQ ID NO:1).

3. Please replace the paragraph beginning at line 12 on page 16 with the following rewritten paragraph:

In addition to the sugarcane OMT promoter having the nucleotide sequence set forth as -3012 to -1 in FIGURE 1 (SEQ ID NO:1), the present invention is directed to other promoter sequences which correspond to the same gene, i.e., a homolog, in other plant species. As defined herein, such related sequences which direct stem-regulated or defense-inducible expression, may be described in terms of their percent homology or identity on a nucleotide level to the nucleotide sequence (-3012 to -1) as set forth in FIGURE 1 (nucleotides 1 to 3012 of SEQ ID NO:1). Alternatively, such related sequences from other plant species may be defined in terms of their ability to hybridize to the OMT promoter of SEQ ID NO: 1 under stringent hybridization conditions.

4. Please replace the paragraph beginning at line 15 on page 17 with the following rewritten paragraph:

Promoter sequences of the present invention may also be described in terms of percent homology or identity on a nucleotide level to the nucleotide sequence -3012 to -1 depicted in FIGURE 1 (nucleotides 1 to 3012 of SEQ ID NO:1). There are a number of computer programs that compare and align nucleic acid sequences which one skilled in the art may use for purposes of determining sequence identity (sequence similarity).